Figure 1: 161P2F10B SSH sequence of 182 nucleotides

```
  1 GATCACACAT TAGGTTATNG ACTTCAATAT TTTCAAATGG TTCAACTTCA GTCTTCTCTT
 61 TAAAACTGGG TCCATGTGCC AAGAAAGATA GCCTCCATGC TCCTAAACTC ATTGTTATAA
121 CCATGGTTGC CTCCTCCACA ATTTGTATTT GATTTACTCC TAACAGCCAG CCACTGTTGA
181 TC
```

Figure 2.

Figure 2A. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 161P2F10B. The 3858 nucleotide sequence of 161P2F10B is shown. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 44-2671 including the stop codon.

```
   1                                                   M  E  S  T  L  T
   1 ctactttattctgataaaacaggtctatgcagctaccaggacaATGGAATCTACGTTGAC
   7  L  A  T  E  Q  P  V  K  K  N  T  L  K  K  Y  K  I  A  C  I
  61 TTTAGCAACGGAACAACCTGTTAAGAAGAACACTCTTAAGAAATATAAAATAGCTTGCAT
  27  V  L  L  A  L  L  V  I  M  S  L  G  L  G  L  G  L  G  L  R
 121 TGTTCTTCTTGCTTTGCTGGTGATCATGTCACTTGGATTAGGCCTGGGGCTTGGACTCAG
  47  K  L  E  K  Q  G  S  C  R  K  K  C  F  D  A  S  F  R  G  L
 181 GAAACTGGAAAAGCAAGGCAGCTGCAGGAAGAAGTGCTTTGATGCATCATTTAGAGGACT
  67  E  N  C  R  C  D  V  A  C  K  D  R  G  D  C  C  W  D  F  E
 241 GGAGAACTGCCGGTGTGATGTGGCATGTAAAGACCGAGGTGATTGCTGCTGGGATTTTGA
  87  D  T  C  V  E  S  T  R  I  W  M  C  N  K  F  R  C  G  E  T
 301 AGACACCTGTGTGGAATCAACTCGAATATGGATGTGCAATAAATTTCGTTGTGGAGAGAC
 107  R  L  E  A  S  L  C  S  C  S  D  D  C  L  Q  K  K  D  C  C
 361 CAGATTAGAGGCCAGCCTTTGCTCTTGTTCAGATGACTGTTTGCAGAAGAAAGATTGCTG
 127  A  D  Y  K  S  V  C  Q  G  E  T  S  W  L  E  E  N  C  D  T
 421 TGCTGACTATAAGAGTGTTTGCCAAGGAGAAACCTCATGGCTGGAAGAAAACTGTGACAC
 147  A  Q  Q  S  Q  C  P  E  G  F  D  L  P  P  V  I  L  F  S  M
 481 AGCCCAGCAGTCTCAGTGCCCAGAAGGGTTTGACCTGCCACCAGTTATCTTGTTTTCTAT
 167  D  G  F  R  A  E  Y  L  Y  T  W  D  T  L  M  P  N  I  N  K
 541 GGATGGATTTAGAGCTGAATATTTATACACATGGGATACTTTAATGCCAAATATCAATAA
 187  L  K  T  C  G  I  H  S  K  Y  M  R  A  M  Y  P  T  K  T  F
 601 ACTGAAAACATGTGGAATTCATTCAAAATACATGAGAGCTATGTATCCTACCAAAACCTT
 207  P  N  H  Y  T  I  V  T  G  L  Y  P  E  S  H  G  I  I  D  N
 661 CCCAAATCATTACACCATTGTCACGGGCTTGTATCCAGAGTCACATGGCATCATTGACAA
 227  N  M  Y  D  V  N  L  N  K  N  F  S  L  S  S  K  E  Q  N  N
 721 TAATATGTATGATGTAAATCTCAACAAGAATTTTTCACTTTCTTCAAAGGAACAAAATAA
 247  P  A  W  W  H  G  Q  P  M  W  L  T  A  M  Y  Q  G  L  K  A
 781 TCCAGCCTGGTGGCATGGGCAACCAATGTGGCTGACAGCAATGTATCAAGGTTTAAAAGC
 267  A  T  Y  F  W  P  G  S  E  V  A  I  N  G  S  F  P  S  I  Y
 841 CGCTACCTACTTTTGGCCCGGATCAGAAGTGGCTATAAATGGCTCCTTTCCTTCCATATA
 287  M  P  Y  N  G  S  V  P  F  E  E  R  I  S  T  L  L  K  W  L
```

901 CATGCCTTACAACGGAAGTGTCCCATTTGAAGAGAGGATTTCTACACTGTTAAAATGGCT

307 D L P K A E R P R F Y T M Y F E E P D S

961 GGACCTGCCCAAAGCTGAAAGACCCAGGTTTTATACCATGTATTTTGAAGAACCTGATTC

327 S G H A G G P V S A R V I K A L Q V V D

1021 CTCTGGACATGCAGGTGGACCAGTCAGTGCCAGAGTAATTAAAGCCTTACAGGTAGTAGA

347 H A F G M L M E G L K Q R N L H N C V N

1081 TCATGCTTTTGGGATGTTGATGGAAGGCCTGAAGCAGCGGAATTTGCACAACTGTGTCAA

367 I I L L A D H G M D Q T Y C N K M E Y M

1141 TATCATCCTTCTGGCTGACCATGGAATGGACCAGACTTATTGTAACAAGATGGAATACAT

387 T D Y F P R I N F F Y M Y E G P A P R I

1201 GACTGATTATTTTCCCAGAATAAACTTCTTCTACATGTACGAAGGGCCTGCCCCCCGCAT

407 R A H N I P H D F F S F N S E E I V R N

1261 CCGAGCTCATAATATACCTCATGACTTTTTTAGTTTTAATTCTGAGGAAATTGTTAGAAA

427 L S C R K P D Q H F K P Y L T P D L P K

1321 CCTCAGTTGCCGAAAACCTGATCAGCATTTCAAGCCCTATTTGACTCCTGATTTGCCAAA

447 R L H Y A K N V R I D K V H L F V D Q Q

1381 GCGACTGCACTATGCCAAGAACGTCAGAATCGACAAAGTTCATCTCTTTGTGGATCAACA

467 W L A V R S K S N T N C G G G N H G Y N

1441 GTGGCTGGCTGTTAGGAGTAAATCAAATACAAATTGTGGAGGAGGCAACCATGGTTATAA

487 N E F R S M E A I F L A H G P S F K E K

1501 CAATGAGTTTAGGAGCATGGAGGCTATCTTTCTGGCACATGGACCCAGTTTTAAAGAGAA

507 T E V E P F E N I E V Y N L M C D L L R

1561 GACTGAAGTTGAACCATTTGAAAATATTGAAGTCTATAACCTAATGTGTGATCTTCTACG

527 I Q P A P N N G T H G S L N H L L K V P

1621 CATTCAACCAGCACCAAACAATGGAACCCATGGTAGTTTAAACCATCTTCTGAAGGTGCC

547 F Y E P S H A E E V S K F S V C G F A N

1681 TTTTTATGAGCCATCCCATGCAGAGGAGGTGTCAAAGTTTTCTGTTTGTGGCTTTGCTAA

567 P L P T E S L D C F C P H L Q N S T Q L

1741 TCCATTGCCCACAGAGTCTCTTGACTGTTTCTGCCCTCACCTACAAAATAGTACTCAGCT

587 E Q V N Q M L N L T Q E E I T A T V K V

1801 GGAACAAGTGAATCAGATGCTAAATCTCACCCAAGAAGAAATAACAGCAACAGTGAAAGT

607 N L P F G R P R V L Q K N V D H C L L Y

1861 AAATTTGCCATTTGGGAGGCCTAGGGTACTGCAGAAGAACGTGGACCACTGTCTCCTTTA

627 H R E Y V S G F G K A M R M P M W S S Y

1921 CCACAGGGAATATGTCAGTGGATTTGGAAAAGCTATGAGGATGCCCATGTGGAGTTCATA

647 T V P Q L G D T S P L P P T V P D C L R

1981 CACAGTCCCCCAGTTGGGAGACACATCGCCTCTGCCTCCCACTGTCCCAGACTGTCTGCG

667 A D V R V P P S E S Q K C S F Y L A D K

2041 GGCTGATGTCAGGGTTCCTCCTTCTGAGAGCCAAAAATGTTCCTTCTATTTAGCAGACAA

687 N I T H G F L Y P P A S N R T S D S Q Y

2101 GAATATCACCCACGGCTTCCTCTATCCTCCTGCCAGCAATAGAACATCAGATAGCCAATA

707 D A L I T S N L V P M Y E E F R K M W D

2161 TGATGCTTTAATTACTAGCAATTTGGTACCTATGTATGAAGAATTCAGAAAAATGTGGGA

727 Y F H S V L L I K H A T E R N G V N V V

2221 CTACTTCCACAGTGTTCTTCTTATAAAACATGCCACAGAAAGAAATGGAGTAAATGTGGT

747 S G P I F D Y N Y D G H F D A P D E I T

2281 TAGTGGACCAATATTTGATTATAATTATGATGGCCATTTTGATGCTCCAGATGAAATTAC

767 K H L A N T D V P I P T H Y F V V L T S

2341 CAAACATTTAGCCAACACTGATGTTCCCATCCCAACACACTACTTTGTGGTGCTGACCAG

787 C K N K S H T P E N C P G W L D V L P F

2401 TTGTAAAAACAAGAGCCACACACCGGAAAACTGCCCTGGGTGGCTGGATGTCCTACCCTT

807 I I P H R P T N V E S C P E G K P E A L

2461 TATCATCCCTCACCGACCTACCAACGTGGAGAGCTGTCCTGAAGGTAAACCAGAAGCTCT

827 W V E E R F T A H I A R V R D V E L L T

2521 TTGGGTTGAAGAAAGATTTACAGCTCACATTGCCCGGGTCCGTGATGTAGAACTTCTCAC

847 G L D F Y Q D K V Q P V S E I L Q L K T

2581 TGGGCTTGACTTCTATCAGGATAAAGTGCAGCCTGTCTCTGAAATTTTGCAACTAAAGAC

867 Y L P T F E T T I *

2641 ATATTTACCAACATTTGAAACCACTATTTAActtaataatgtctacttaatatataattt

2701 actgtataaagtaattttggcaaaatataagtgatttttttctggagaattgtaaaataaa

2761 gttttctatttttccttaaaaaaaaaaccggaattccgggcttgggaggctgaggcagga

2821 gactcgcttgaacccgggaggcagaggttgcagtgagccaagattgcgccattgcactcc

2881 agagcctgggtgacagagcaagactacatctcaaaaaataaataaataaaataaaagtaa

2941 caataaaaataaaaagaacagcagagagaatgagcaaggagaaatgtcacaaactattgc

3001 aaaatactgttacactgggttggctctccaagaagatactggaatctcttcagccatttg

3061 cttttcagaagtagaaaccagcaaaccacctctaagcggagaacatacgattctttatta

3121 agtagctctggggaaggaaagaataaaagttgatagctccctgattgggaaaaaatgcac

3181 aattaataaagaatgaagatgaaagaaagcatgcttatgttgtaacacaaaaaaaattca

3241 caaacgttggtggaaggaaaacagtatagaaaacattactttaactaaaagctggaaaaa

3301 ttttcagttgggatgcgactgacaaaaagaacgggatttccaggcataaagttggcgtga

3361 gctacagagggcaccatgtggctcagtggaagacccttcaagattcaaagttccatttga

3421 cagagcaaaggcacttcgcaaggagaagggtttaaattatgggtccaaaagccaagtggt

3481 aaagcgagcaatttgcagcataactgcttctcctagacagggctgagtgggcaaaatacg

3541 acagtacacacagtgactattagccactgccagaaacaggctgaacagccctgggagaca

3601 agggaaggcaggtggtgggagttgttcatggagagaaaggagagttttagaaccagcaca

3661 tccactggagatgctgggccaccagacccctcccagtcaataaagtctggtgcctcattt

```
3721 gatctcagcctcatcatgaccctggagagaccctgataccatctgccagtccccgacagc
3781 ttaggcactccttgccatcaacctgacccccgagtggttctccaggctccctgccccac
3841 ccattcaggccggaattc
```

Figure 2B: The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 161P2F10B variant 1. The 3858 nucleotide sequence of 161P2F10B variant 1 is shown. The start methionine is underlined. The open reading frame extends from nucleic acid 44-2671 including the stop codon.

```
  1                                                  M  E  S  T  L  T
  1 ctactttattctgataaaacaggtctatgcagctaccaggacaATGGAATCTACGTTGAC
  7  L  A  T  E  Q  P  V  K  K  N  T  L  K  K  Y  K  I  A  C  I
 61 TTTAGCAACGGAACAACCTGTTAAGAAGAACACTCTTAAGAAATATAAAATAGCTTGCAT
 27  V  L  L  A  L  L  V  I  M  S  L  G  L  G  L  G  L  G  L  R
121 TGTTCTTCTTGCTTTGCTGGTGATCATGTCACTTGGATTAGGCCTGGGGCTTGGACTCAG
 47  K  L  E  K  Q  G  S  C  R  K  K  C  F  D  A  S  F  R  G  L
181 GAAACTGGAAAAGCAAGGCAGCTGCAGGAAGAAGTGCTTTGATGCATCATTTAGAGGACT
 67  E  N  C  R  C  D  V  A  C  K  D  R  G  D  C  C  W  D  F  E
241 GGAGAACTGCCGGTGTGATGTGGCATGTAAAGACCGAGGTGATTGCTGCTGGGATTTTGA
 87  D  T  C  V  E  S  T  R  I  W  M  C  N  K  F  R  C  G  E  T
301 AGACACCTGTGTGGAATCAACTCGAATATGGATGTGCAATAAATTTCGTTGTGGAGAGAC
107  R  L  E  A  S  L  C  S  C  S  D  D  C  L  Q  R  K  D  C  C
361 CAGATTAGAGGCCAGCCTTTGCTCTTGTTCAGATGACTGTTTGCAGAGGAAAGATTGCTG
127  A  D  Y  K  S  V  C  Q  G  E  T  S  W  L  E  E  N  C  D  T
421 TGCTGACTATAAGAGTGTTTGCCAAGGAGAAACCTCATGGCTGGAAGAAAACTGTGACAC
147  A  Q  Q  S  Q  C  P  E  G  F  D  L  P  P  V  I  L  F  S  M
481 AGCCCAGCAGTCTCAGTGCCCAGAAGGGTTTGACCTGCCACCAGTTATCTTGTTTTCTAT
167  D  G  F  R  A  E  Y  L  Y  T  W  D  T  L  M  P  N  I  N  K
541 GGATGGATTTAGAGCTGAATATTTATACACATGGGATACTTTAATGCCAAATATCAATAA
187  L  K  T  C  G  I  H  S  K  Y  M  R  A  M  Y  P  T  K  T  F
601 ACTGAAAACATGTGGAATTCATTCAAAATACATGAGAGCTATGTATCCTACCAAAACCTT
207  P  N  H  Y  T  I  V  T  G  L  Y  P  E  S  H  G  I  I  D  N
661 CCCAAATCATTACACCATTGTCACGGGCTTGTATCCAGAGTCACATGGCATCATTGACAA
227  N  M  Y  D  V  N  L  N  K  N  F  S  L  S  S  K  E  Q  N  N
721 TAATATGTATGATGTAAATCTCAACAAGAATTTTTCACTTTCTTCAAAGGAACAAAATAA
247  P  A  W  W  H  G  Q  P  M  W  L  T  A  M  Y  Q  G  L  K  A
781 TCCAGCCTGGTGGCATGGGCAACCAATGTGGCTGACAGCAATGTATCAAGGTTTAAAAGC
267  A  T  Y  F  W  P  G  S  E  V  A  I  N  G  S  F  P  S  I  Y
841 CGCTACCTACTTTTGGCCCGGATCAGAAGTGGCTATAAATGGCTCCTTTCCTTCCATATA
287  M  P  Y  N  G  S  V  P  F  E  E  R  I  S  T  L  L  K  W  L
901 CATGCCTTACAACGGAAGTGTCCCATTTGAAGAGAGGATTTCTACACTGTTAAAATGGCT
```

307 D L P K A E R P R F Y T M Y F E E P D S

961 GGACCTGCCCAAAGCTGAAAGACCCAGGTTTTATACCATGTATTTTGAAGAACCTGATTC

327 S G H A G G P V S A R V I K A L Q V V D

1021 CTCTGGACATGCAGGTGGACCAGTCAGTGCCAGAGTAATTAAAGCCTTACAGGTAGTAGA

347 H A F G M L M E G L K Q R N L H N C V N

1081 TCATGCTTTTGGGATGTTGATGGAAGGCCTGAAGCAGCGGAATTTGCACAACTGTGTCAA

367 I I L L A D H G M D Q T Y C N K M E Y M

1141 TATCATCCTTCTGGCTGACCATGGAATGGACCAGACTTATTGTAACAAGATGGAATACAT

387 T D Y F P R I N F F Y M Y E G P A P R I

1201 GACTGATTATTTTCCCAGAATAAACTTCTTCTACATGTACGAAGGGCCTGCCCCCCGCAT

407 R A H N I P H D F F S F N S E E I V R N

1261 CCGAGCTCATAATATACCTCATGACTTTTTTAGTTTTAATTCTGAGGAAATTGTTAGAAA

427 L S C R K P D Q H F K P Y L T P D L P K

1321 CCTCAGTTGCCGAAAACCTGATCAGCATTTCAAGCCCTATTTGACTCCTGATTTGCCAAA

447 R L H Y A K N V R I D K V H L F V D Q Q

1381 GCGACTGCACTATGCCAAGAACGTCAGAATCGACAAAGTTCATCTCTTTGTGGATCAACA

467 W L A V R S K S N T N C G G G N H G Y N

1441 GTGGCTGGCTGTTAGGAGTAAATCAAATACAAATTGTGGAGGAGGCAACCATGGTTATAA

487 N E F R S M E A I F L A H G P S F K E K

1501 CAATGAGTTTAGGAGCATGGAGGCTATCTTTCTGGCACATGGACCCAGTTTTAAAGAGAA

507 T E V E P F E N I E V Y N L M C D L L R

1561 GACTGAAGTTGAACCATTTGAAAATATTGAAGTCTATAACCTAATGTGTGATCTTCTACG

527 I Q P A P N N G T H G S L N H L L K V P

1621 CATTCAACCAGCACCAAACAATGGAACCCATGGTAGTTTAAACCATCTTCTGAAGGTGCC

547 F Y E P S H A E E V S K F S V C G F A N

1681 TTTTTATGAGCCATCCCATGCAGAGGAGGTGTCAAAGTTTTCTGTTTGTGGCTTTGCTAA

567 P L P T E S L D C F C P H L Q N S T Q L

1741 TCCATTGCCCACAGAGTCTCTTGACTGTTTCTGCCCTCACCTACAAAATAGTACTCAGCT

587 E Q V N Q M L N L T Q E E I T A T V K V

1801 GGAACAAGTGAATCAGATGCTAAATCTCACCCAAGAAGAAATAACAGCAACAGTGAAAGT

607 N L P F G R P R V L Q K N V D H C L L Y

1861 AAATTTGCCATTTGGGAGGCCTAGGGTACTGCAGAAGAACGTGGACCACTGTCTCCTTTA

627 H R E Y V S G F G K A M R M P M W S S Y

1921 CCACAGGGAATATGTCAGTGGATTTGGAAAAGCTATGAGGATGCCCATGTGGAGTTCATA

647 T V P Q L G D T S P L P P T V P D C L R

1981 CACAGTCCCCCAGTTGGGAGACACATCGCCTCTGCCTCCCACTGTCCCAGACTGTCTGCG

667 A D V R V P P S E S Q K C S F Y L A D K

2041 GGCTGATGTCAGGGTTCCTCCTTCTGAGAGCCAAAAATGTTCCTTCTATTTAGCAGACAA

687 N I T H G F L Y P P A S N R T S D S Q Y

2101 GAATATCACCCACGGCTTCCTCTATCCTCCTGCCAGCAATAGAACATCAGATAGCCAATA

707 D A L I T S N L V P M Y E E F R K M W D

2161 TGATGCTTTAATTACTAGCAATTTGGTACCTATGTATGAAGAATTCAGAAAAATGTGGGA

727 Y F H S V L L I K H A T E R N G V N V V
2221 CTACTTCCACAGTGTTCTTCTTATAAAACATGCCACAGAAAGAAATGGAGTAAATGTGGT
747 S G P I F D Y N Y D G H F D A P D E I T
2281 TAGTGGACCAATATTTGATTATAATTATGATGGCCATTTTGATGCTCCAGATGAAATTAC
767 K H L A N T D V P I P T H Y F V V L T S
2341 CAAACATTTAGCCAACACTGATGTTCCCATCCCAACACACTACTTTGTGGTGCTGACCAG
787 C K N K S H T P E N C P G W L D V L P F
2401 TTGTAAAAACAAGAGCCACACACCGGAAAACTGCCCTGGGTGGCTGGATGTCCTACCCTT
807 I I P H R P T N V E S C P E G K P E A L
2461 TATCATCCCTCACCGACCTACCAACGTGGAGAGCTGTCCTGAAGGTAAACCAGAAGCTCT
827 W V E E R F T A H I A R V R D V E L L T
2521 TTGGGTTGAAGAAAGATTTACAGCTCACATTGCCCGGGTCCGTGATGTAGAACTTCTCAC
847 G L D F Y Q D K V Q P V S E I L Q L K T
2581 TGGGCTTGACTTCTATCAGGATAAAGTGCAGCCTGTCTCTGAAATTTTGCAACTAAAGAC
867 Y L P T F E T T I *
2641 ATATTTACCAACATTTGAAACCACTATTTAActtaataatgtctacttaatatataattt
2701 actgtataaagtaattttggcaaaatataagtgatttttctggagaattgtaaaataaa
2761 gttttctatttttccttaaaaaaaaaaccggaattccgggcttgggaggctgaggcagga
2821 gactcgcttgaacccgggaggcagaggttgcagtgagccaagattgcgccattgcactcc
2881 agagcctgggtgacagagcaagactacatctcaaaaaataaataaataaaataaaagtaa
2941 caataaaaataaaaagaacagcagagagaatgagcaaggagaaatgtcacaaactattgc
3001 aaaatactgttacactgggttggctctccaagaagatactggaatctcttcagccatttg
3061 cttttcagaagtagaaaccagcaaaccacctctaagcggagaacatacgattctttatta
3121 agtagctctggggaaggaaagaataaaagttgatagctccctgattgggaaaaaatgcac
3181 aattaataaagaatgaagatgaaagaaagcatgcttatgttgtaacacaaaaaaaattca
3241 caaacgttggtggaaggaaaacagtatagaaaacattactttaactaaaagctggaaaaa
3301 ttttcagttgggatgcgactgacaaaaagaacgggatttccaggcataaagttggcgtga
3361 gctacagagggcaccatgtggctcagtggaagaccccttcaagattcaaagttccatttga
3421 cagagcaaaggcacttcgcaaggagaagggtttaaattatgggtccaaaagccaagtggt
3481 aaagcgagcaatttgcagcataactgcttctcctagacagggctgagtgggcaaaatacg
3541 acagtacacacagtgactattagccactgccagaaacaggctgaacagccctgggagaca
3601 agggaaggcaggtggtgggagttgttcatggagagaaaggagagttttagaaccagcaca
3661 tccactggagatgctgggccaccagacccctcccagtcaataaagtctggtgcctcattt
3721 gatctcagcctcatcatgaccctggagagaccctgataccatctgccagtccccgacagc
3781 ttaggcactccttgccatcaacctgaccccccgagtggttctccaggctccctgccccac
3841 ccattcaggccggaattc

Figure 3A. Amino acid sequence of 161P2F10B (SEQ ID. NO. :____). The 161P2F10B protein has 875 amino acids.

```
  1 MESTLTLATE QPVKKNTLKK YKIACIVLLA LLVIMSLGLG LGLGLRKLEK QGSCRKKCFD
 61 ASFRGLENCR CDVACKDRGD CCWDFEDTCV ESTRIWMCNK FRCGETRLEA SLCSCSDDCL
121 QKKDCCADYK SVCQGETSWL EENCDTAQQS QCPEGFDLPP VILFSMDGFR AEYLYTWDTL
181 MPNINKLKTC GIHSKYMRAM YPTKTFPNHY TIVTGLYPES HGIIDNNMYD VNLNKNFSLS
241 SKEQNNPAWW HGQPMWLTAM YQGLKAATYF WPGSEVAING SFPSIYMPYN GSVPFEERIS
301 TLLKWLDLPK AERPRFYTMY FEEPDSSGHA GGPVSARVIK ALQVVDHAFG MLMEGLKQRN
361 LHNCVNIILL ADHGMDQTYC NKMEYMTDYF PRINFFYMYE GPAPRIRAHN IPHDFFSFNS
421 EEIVRNLSCR KPDQHFKPYL TPDLPKRLHY AKNVRIDKVH LFVDQQWLAV RSKSNTNCGG
481 GNHGYNNEFR SMEAIFLAHG PSFKEKTEVE PFENIEVYNL MCDLLRIQPA PNNGTHGSLN
541 HLLKVPFYEP SHAEEVSKFS VCGFANPLPT ESLDCFCPHL QNSTQLEQVN QMLNLTQEEI
601 TATVKVNLPF GRPRVLQKNV DHCLLYHREY VSGFGKAMRM PMWSSYTVPQ LGDTSPLPPT
661 VPDCLRADVR VPPSESQKCS FYLADKNITH GFLYPPASNR TSDSQYDALI TSNLVPMYEE
721 FRKMWDYFHS VLLIKHATER NGVNVVSGPI FDYNYDGHFD APDEITKHLA NTDVPIPTHY
781 FVVLTSCKNK SHTPENCPGW LDVLPFIIPH RPTNVESCPE GKPEALWVEE RFTAHIARVR
841 DVELLTGLDF YQDKVQPVSE ILQLKTYLPT FETTI
```

Figure 3B. Amino acid sequence of 161P2F10B variant 1 (SEQ ID. NO. :____). The 161P2F10B variant 1 protein has 875 amino acids.

```
  1 MESTLTLATE QPVKKNTLKK YKIACIVLLA LLVIMSLGLG LGLGLRKLEK QGSCRKKCFD
 61 ASFRGLENCR CDVACKDRGD CCWDFEDTCV ESTRIWMCNK FRCGETRLEA SLCSCSDDCL
121 QRKDCCADYK SVCQGETSWL EENCDTAQQS QCPEGFDLPP VILFSMDGFR AEYLYTWDTL
181 MPNINKLKTC GIHSKYMRAM YPTKTFPNHY TIVTGLYPES HGIIDNNMYD VNLNKNFSLS
241 SKEQNNPAWW HGQPMWLTAM YQGLKAATYF WPGSEVAING SFPSIYMPYN GSVPFEERIS
301 TLLKWLDLPK AERPRFYTMY FEEPDSSGHA GGPVSARVIK ALQVVDHAFG MLMEGLKQRN
361 LHNCVNIILL ADHGMDQTYC NKMEYMTDYF PRINFFYMYE GPAPRIRAHN IPHDFFSFNS
421 EEIVRNLSCR KPDQHFKPYL TPDLPKRLHY AKNVRIDKVH LFVDQQWLAV RSKSNTNCGG
481 GNHGYNNEFR SMEAIFLAHG PSFKEKTEVE PFENIEVYNL MCDLLRIQPA PNNGTHGSLN
541 HLLKVPFYEP SHAEEVSKFS VCGFANPLPT ESLDCFCPHL QNSTQLEQVN QMLNLTQEEI
601 TATVKVNLPF GRPRVLQKNV DHCLLYHREY VSGFGKAMRM PMWSSYTVPQ LGDTSPLPPT
661 VPDCLRADVR VPPSESQKCS FYLADKNITH GFLYPPASNR TSDSQYDALI TSNLVPMYEE
721 FRKMWDYFHS VLLIKHATER NGVNVVSGPI FDYNYDGHFD APDEITKHLA NTDVPIPTHY
781 FVVLTSCKNK SHTPENCPGW LDVLPFIIPH RPTNVESCPE GKPEALWVEE RFTAHIARVR
841 DVELLTGLDF YQDKVQPVSE ILQLKTYLPT FETTI
```

Figure 4

Figure 4A. Amino acid alignment of 161P2F10B with ENPP3.

```
161P2F10B   m e s t l t l a t e q p v k k n t l k k y k i a c i v l l a l l v i m s l g l g   40
    ENPP3   m e s t l t l a t e q p v k k n t l k k y k i a c i v l l a l l v i m s l g l g   40

161P2F10B   l g l g l r k l e k q g s c r k k c f d a s f r g l e n c r c d v a c k d r g d   80
    ENPP3   l g l g l r k l e k q g s c r k k c f d a s f r g l e n c r c d v a c k d r g d   80

161P2F10B   c c w d f e d t c v e s t r i w m c n k f r c g e t r l e a s l c s c s d d c l   120
    ENPP3   c c w d f e d t c v e s t r i w m c n k f r c g e t r l e a s l c s c s d d c l   120

161P2F10B   q k k d c c a d y k s v c q g e t s w l e e n c d t a q q s q c p e g f d l p p   160
    ENPP3   q k k d c c a d y k s v c q g e t s w l e e n c d t a q q s q c p e g f d l p p   160

161P2F10B   v i l|f s m d g f r a e y l y t w d t l m p n i n k l k t c g i h s k y m r a m   200
    ENPP3   v i l f s m d g f r a e y l y t w d t l m p n i n k l k t c g i h s k y m r a m   200

161P2F10B   y p t k t f p n h y t i v t g l y p e s h g i i d n n m y d v n l n k n f s l s   240
    ENPP3   y p t k t f p n h y t i v t g l y p e s h g i i d n n m y d v n l n k n f s l s   240

161P2F10B   s k e q n n p a w w h g q p m w l t a m y q g l k a a t y f w p g s e v a i n g   280
    ENPP3   s k e q n n p a w w h g q p m w l t a m y q g l k a a t y f w p g s e v a i n g   280

161P2F10B   s f p s i y m p y n g s v p f e e r i s t l l k w l d l p k a e r p r f y t m y   320
    ENPP3   s f p s i y m p y n g s v p f e e r i s t l l k w l d l p k a e r p r f y t m y   320

161P2F10B   f e e p d s s g h a g g p v s a r v i k a l q v v d h a f g m l m e g l k q r n   360
    ENPP3   f e e p d s s g h a g g p v s a r v i k a l q v v d h a f g m l m e g l k q r n   360

161P2F10B   l h n c v n i i l l a d h g m d q t y c n k m e y m t d y f p r i n f f y m y e   400
    ENPP3   l h n r v n i i l l a d h g m d q t y c n k m e y m t d y f p r i n f f y m y e   400

161P2F10B   g p a p r i r a h n i p h d f f s f n s e e i v r n l s c r k p d q h f k p y l   440
    ENPP3   g p a p r i r a h n i p h d f f s f n s e e i v r n l s c r k p d q h f k p y l   440

161P2F10B   t p d l p k r l h y a k n v r i d k v h l f v d q q w l a v r s k s n t n c g g   480
    ENPP3   t p d l p k r l h y a k n v r i d k v h l f v d q q w l a v r s k s n t n c g g   480

161P2F10B   g n h g y n n e f r s m e a i f l a h g p s f k e k t e v e p f e n i e v y n l   520
    ENPP3   g n h g y n n e f r s m e a i f l a h g p s f k e k t e v e p f e n i e v y n l   520

161P2F10B   m c d l l r i q p a p n n g t h g s l n h l l k v p f y e p s h a e e v s k f s   560
    ENPP3   m c d l l r i q p a p n n g t h g s l n h l l k v p f y e p s h a e e v s k f s   560

161P2F10B   v c g f a n p l p t e s l d c f c p h l q n s t q l e q v n q m l n l t q e e i   600
    ENPP3   v c g f a n p l p t e s l d c f c p h l q n s t q l e q v n q m l n l t q e e i   600

161P2F10B   t a t v k v n l p f g r p r v l q k n v d h c l l y h r e y v s g f g k a m r m   640
    ENPP3   t a t v k v n l p f g r p r v l q k n v d h c l l y h r e y v s g f g k a m r m   640

161P2F10B   p m w s s y t v p q l g d t s p l p p t v p d c l r a d v r v p p s e s q k c s   680
    ENPP3   p m w s s y t v p q l g d t s p l p p t v p d c l r a d v r v p p s e s q k c s   680

161P2F10B   f y l a d k n i t h g f l y p p a s n r t s d s q y d a l i t s n l v p m y e e   720
    ENPP3   f y l a d k n i t h g f l y p p a s n r t s d s q y d a l i t s n l v p m y e e   720

161P2F10B   f r k m w d y f h s v l l i k h a t e r n g v n v v s g p i f d y n y d g h f d   760
    ENPP3   f r k m w d y f h s v l l i k h a t e r n g v n v v s g p i f d y n y d g h f d   760

161P2F10B   a p d e i t k h l a n t d v p i p t h y f v v l t s c k n k s h t p e n c p g w   800
    ENPP3   a p d e i t k h l a n t d v p i p t h y f v v l t s c k n k s h t p e n c p g w   800
```

```
161P2F10B  l d v l p f i i p h r p t n v e s c p e g k p e a l w v e e r f t a h i a r v r  840
   ENPP3   l d v l p f i i p h r p t n v e s c p e g k p e a l w v e e r f t a h i a r v r  840

161P2F10B  d v e l l t g l d f y q d k v q p v s e i l q l k t y l p t f e t t i          875
   ENPP3   d v e l l t g l d f y q d k v q p v s e i l q l k t y l p t f e t t i          875
```

Figure 4b. Amino acid alignment of 161P2F10B with 161P2F10B variant 1.

```
          161P2F10B  m e s t l t l a t e q p v k k n t l k k y k i a c i v l l a l l v i m s l g l g   40
161P2F10B variant 1  m e s t l t l a t e q p v k k n t l k k y k i a c i v l l a l l v i m s l g l g   40

          161P2F10B  l g l g l r k l e k q g s c r k k c f d a s f r g l e n c r c d v a c k d r g d   80
161P2F10B variant 1  l g l g l r k l e k q g s c r k k c f d a s f r g l e n c r c d v a c k d r g d   80

          161P2F10B  c c w d f e d t c v e s t r i w m c n k f r c g e t r l e a s l c s c s d d c l   12C
161P2F10B variant 1  c c w d f e d t c v e s t r i w m c n k f r c g e t r l e a s l c s c s d d c l   12C

          161P2F10B  q k k d c c a d y k s v c q g e t s w l e e n c d t a q q s q c p e g f d l p p   16C
161P2F10B variant 1  q r k d c c a d y k s v c q g e t s w l e e n c d t a q q s q c p e g f d l p p   16C

          161P2F10B  v i l f s m d g f r a e y l y t w d t l m p n i n k l k t c g i h s k y m r a m   20C
161P2F10B variant 1  v i l f s m d g f r a e y l y t w d t l m p n i n k l k t c g i h s k y m r a m   20C

          161P2F10B  y p t k t f p n h y t i v t g l y p e s h g i i d n n m y d v n l n k n f s l s   24C
161P2F10B variant 1  y p t k t f p n h y t i v t g l y p e s h g i i d n n m y d v n l n k n f s l s   24C

          161P2F10B  s k e q n n p a w w h g q p m w l t a m y q g l k a a t y f w p g s e v a i n g   28C
161P2F10B variant 1  s k e q n n p a w w h g q p m w l t a m y q g l k a a t y f w p g s e v a i n g   28C

          161P2F10B  s f p s i y m p y n g s v p f e e r i s t l l k w l d l p k a e r p r f y t m y   32C
161P2F10B variant 1  s f p s i y m p y n g s v p f e e r i s t l l k w l d l p k a e r p r f y t m y   32C

          161P2F10B  f e e p d s s g h a g g p v s a r v i k a l q v v d h a f g m l m e g l k q r n   36C
161P2F10B variant 1  f e e p d s s g h a g g p v s a r v i k a l q v v d h a f g m l m e g l k q r n   36C

          161P2F10B  l h n c v n i i l l a d h g m d q t y c n k m e y m t d y f p r i n f f y m y e   40C
161P2F10B variant 1  l h n r v n i i l l a d h g m d q t y c n k m e y m t d y f p r i n f f y m y e   40C

          161P2F10B  g p a p r i r a h n i p h d f f s f n s e e i v r n l s c r k p d q h f k p y l   44C
161P2F10B variant 1  g p a p r i r a h n i p h d f f s f n s e e i v r n l s c r k p d q h f k p y l   44C

          161P2F10B  t p d l p k r l h y a k n v r i d k v h l f v d q q w l a v r s k s n t n c g g   48C
161P2F10B variant 1  t p d l p k r l h y a k n v r i d k v h l f v d q q w l a v r s k s n t n c g g   48C

          161P2F10B  g n h g y n n e f r s m e a i f l a h g p s f k e k t e v e p f e n i e v y n l   52C
161P2F10B variant 1  g n h g y n n e f r s m e a i f l a h g p s f k e k t e v e p f e n i e v y n l   52C

          161P2F10B  m c d l l r i q p a p n n g t h g s l n h l l k v p f y e p s h a e e v s k f s   56C
161P2F10B variant 1  m c d l l r i q p a p n n g t h g s l n h l l k v p f y e p s h a e e v s k f s   56C

          161P2F10B  v c g f a n p l p t e s l d c f c p h l q n s t q l e q v n q m l n l t q e e i   60C
161P2F10B variant 1  v c g f a n p l p t e s l d c f c p h l q n s t q l e q v n q m l n l t q e e i   60C

          161P2F10B  t a t v k v n l p f g r p r v l q k n v d h c l l y h r e y v s g f g k a m r m   64C
161P2F10B variant 1  t a t v k v n l p f g r p r v l q k n v d h c l l y h r e y v s g f g k a m r m   64C

          161P2F10B  p m w s s y t v p q l g d t s p l p p t v p d c l r a d v r v p p s e s q k c s   68C
161P2F10B variant 1  p m w s s y t v p q l g d t s p l p p t v p d c l r a d v r v p p s e s q k c s   68C

          161P2F10B  f y l a d k n i t h g f l y p p a s n r t s d s q y d a l i t s n l v p m y e e   72C
161P2F10B variant 1  f y l a d k n i t h g f l y p p a s n r t s d s q y d a l i t s n l v p m y e e   72C
```

```
          161P2F10B  f r k m w d y f h s v l l i k h a t e r n g v n v v s g p i f d y n y d g h f d  76(
161P2F10B variant 1  f r k m w d y f h s v l l i k h a t e r n g v n v v s g p i f d y n y d g h f d  76(

          161P2F10B  a p d e i t k h l a n t d v p i p t h y f v v l t s c k n k s h t p e n c p g w  80(
161P2F10B variant 1  a p d e i t k h l a n t d v p i p t h y f v v l t s c k n k s h t p e n c p g w  80(

          161P2F10B  l d v l p f i i p h r p t n v e s c p e g k p e a l w v e e r f t a h i a r v r  84(
161P2F10B variant 1  l d v l p f i i p h r p t n v e s c p e g k p e a l w v e e r f t a h i a r v r  84(

          161P2F10B  d v e l l t g l d f y q d k v q p v s e i l q l k t y l p t f e t t i          87(
161P2F10B variant 1  d v e l l t g l d f y q d k v q p v s e i l q l k t y l p t f e t t i          87(
```

4C) Alignment of 161P2F10B and SNP variant 2 carrying a T to P mutation at position 874.

```
Query: 492 MEAIFLAHGPSFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEPS 551
           MEAIFLAHGPSFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEPS
Sbjct: 1   MEAIFLAHGPSFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEPS 60

Query: 552 HAEEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLPFG 611
           HAEEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLPFG
Sbjct: 61  HAEEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLPFG 120

Query: 612 RPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTVPQLGDTSPLPPTVPDCLRADVRV
671
           RPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTVPQLGDTSPLPPTVPDCLRADVRV
Sbjct: 121 RPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTVPQLGDTSPLPPTVPDCLRADVRV 180

Query: 672 PPSESQKCSFYLADKNITHGFLYPPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHSV 731
           PPSESQKCSFYLADKNITHGFLYPPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHSV
Sbjct: 181 PPSESQKCSFYLADKNITHGFLYPPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHSV 240

Query: 732 LLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKS 791
           LLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKS
Sbjct: 241 LLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKS 300

Query: 792 HTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVRDVELLTGLDFY 851
           HTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVRDVELLTGLDFY
Sbjct: 301 HTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVRDVELLTGLDFY 360

Query: 852 QDKVQPVSEILQLKTYLPTFETTI 875
           QDKVQPVSEILQLKTYLPTFET I
Sbjct: 361 QDKVQPVSEILQLKTYLPTFETPI 384
```

Figure 5: 161P2F10B Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

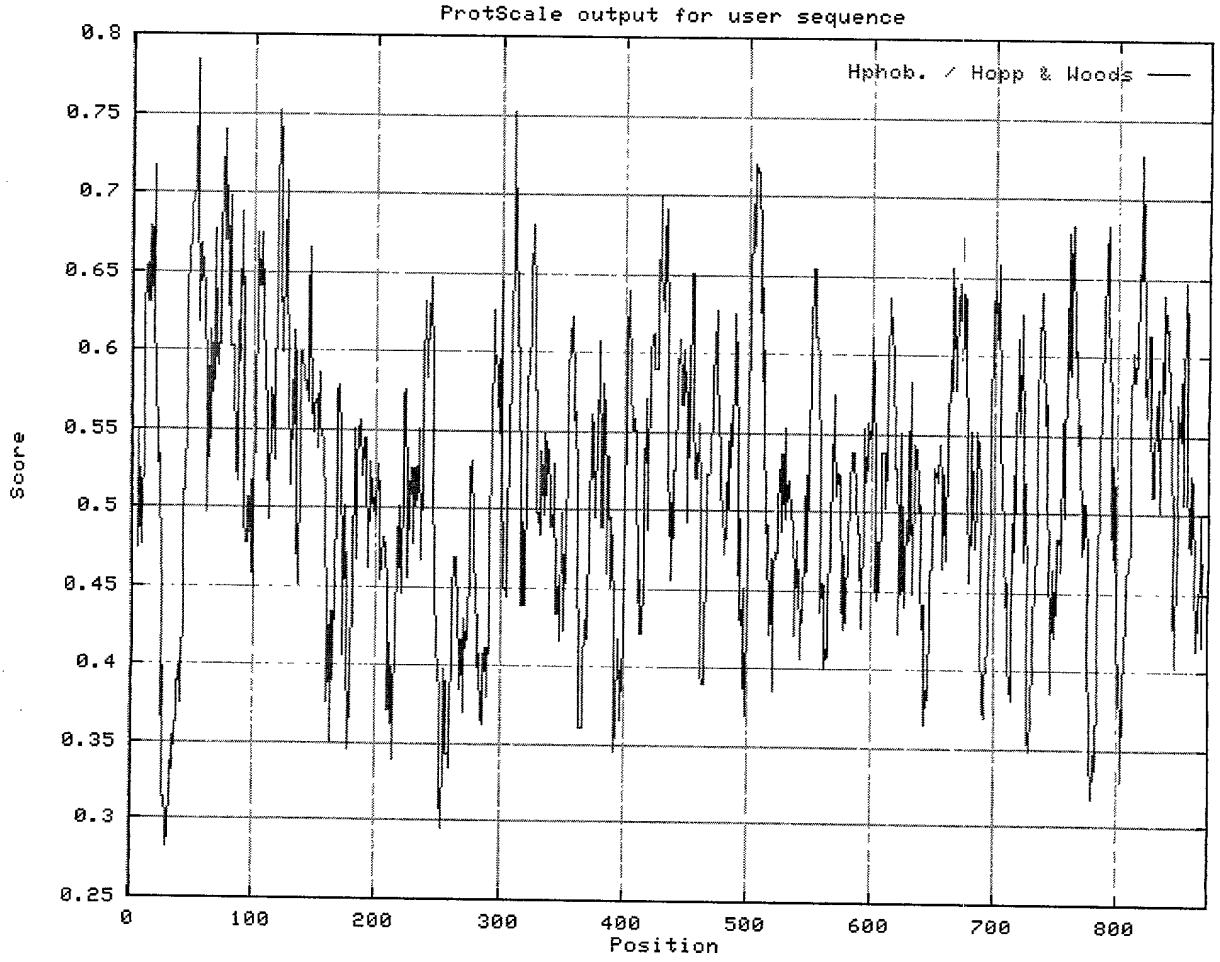


Figure 6: 161P2F10B Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

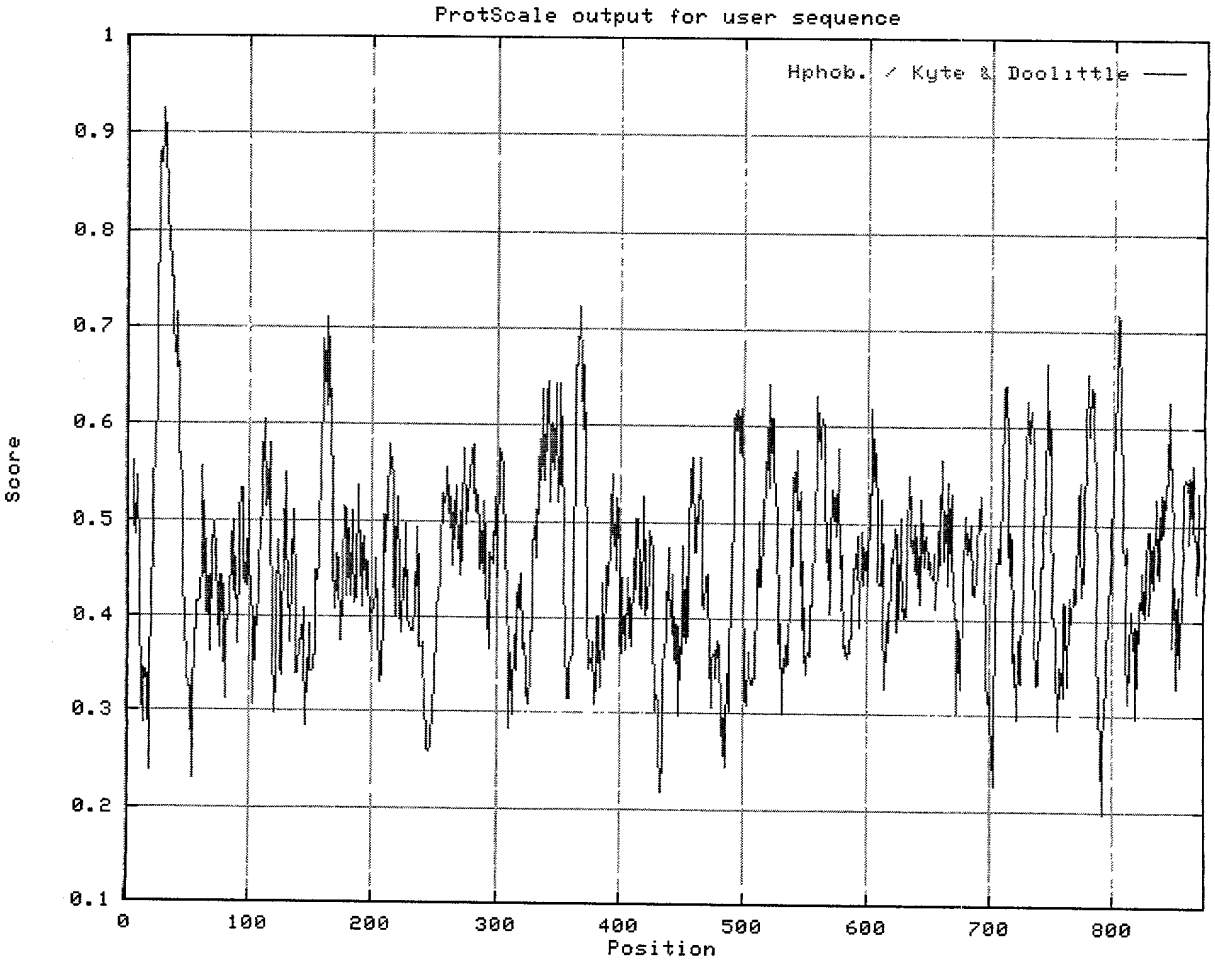


Figure 7: 161P2F10B % Accessible Residues Profile

(Janin J., 1979. Nature 277:491-492)

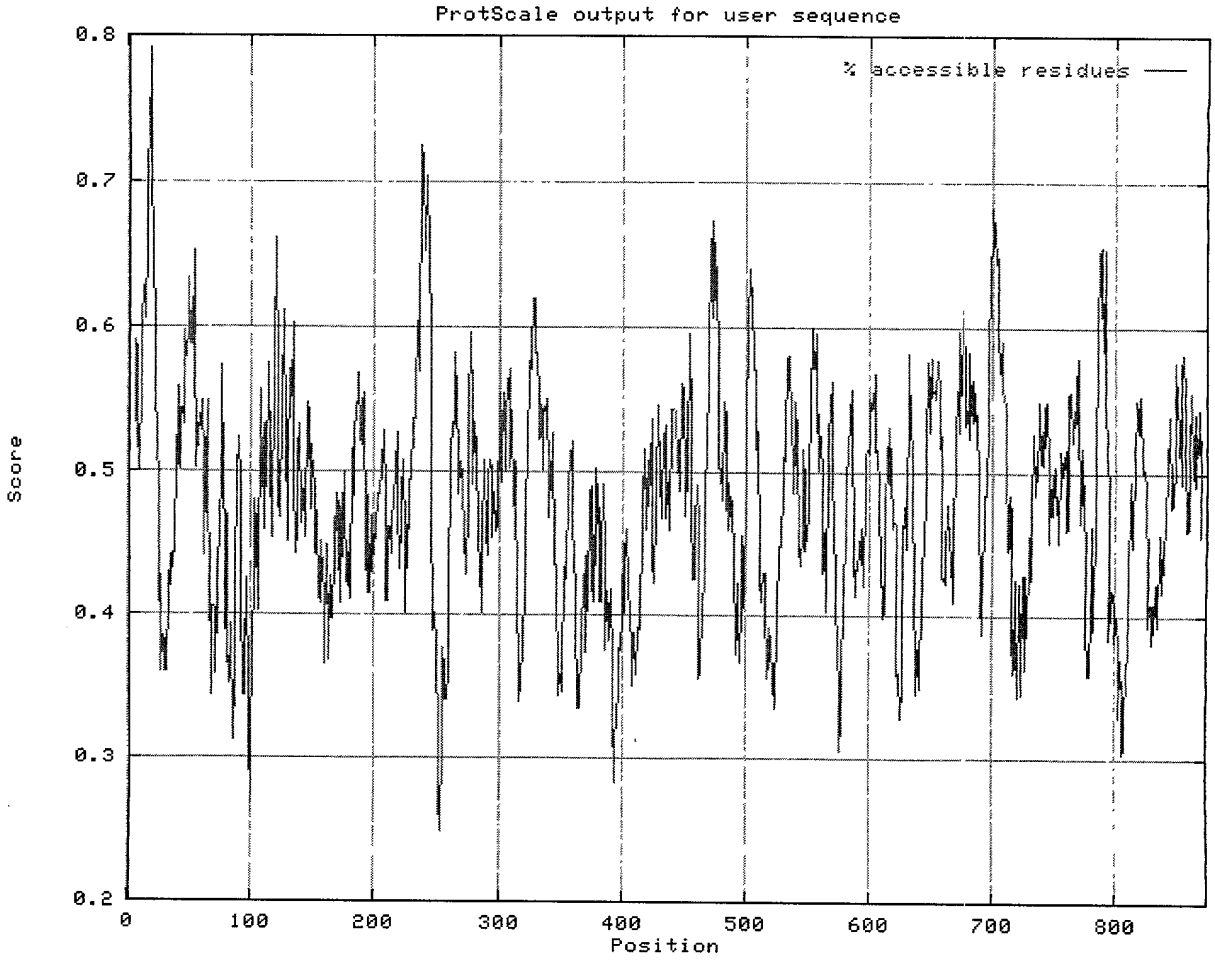


Figure 8: 161P2F10B Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

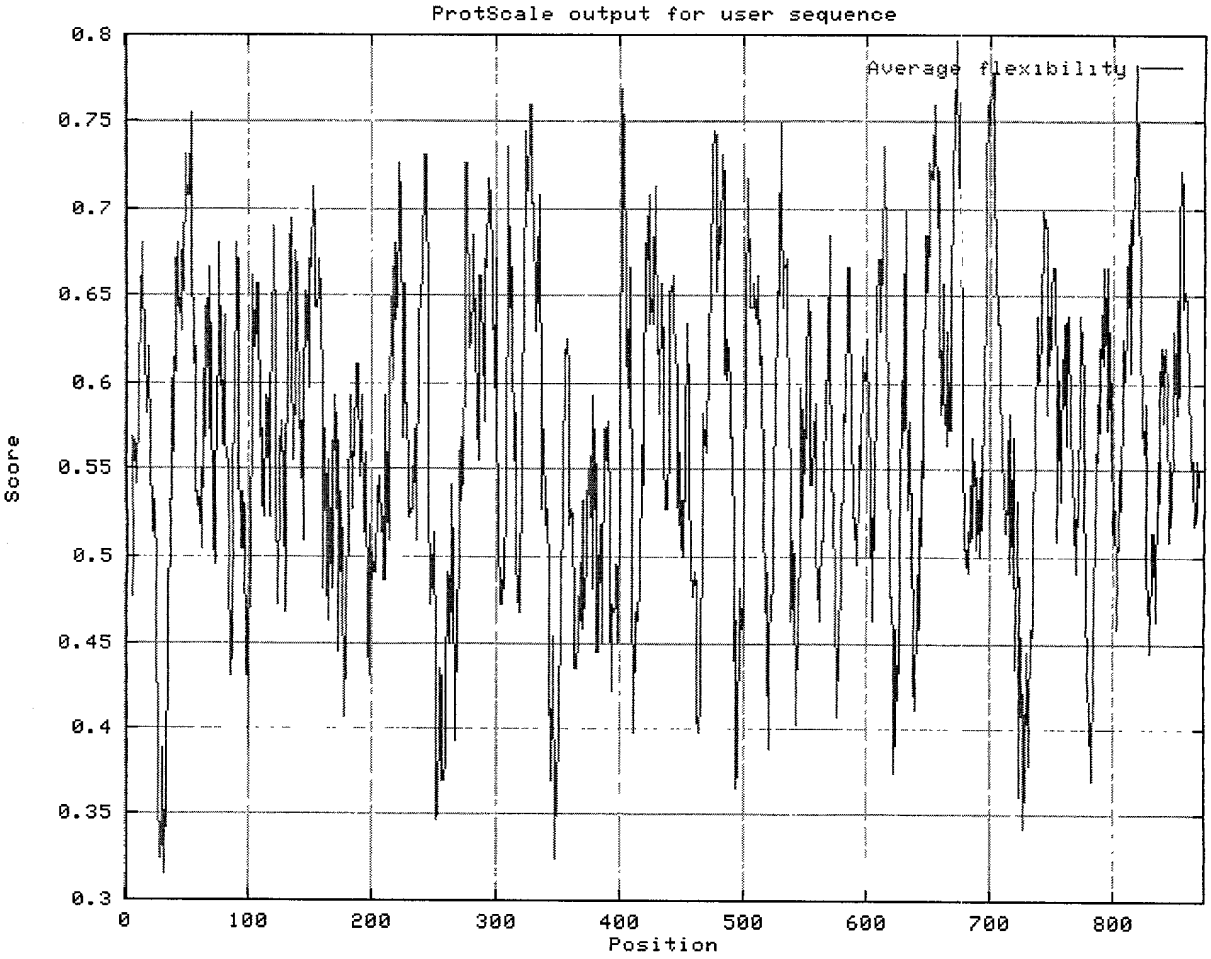


Figure 9: 161P2F10B Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

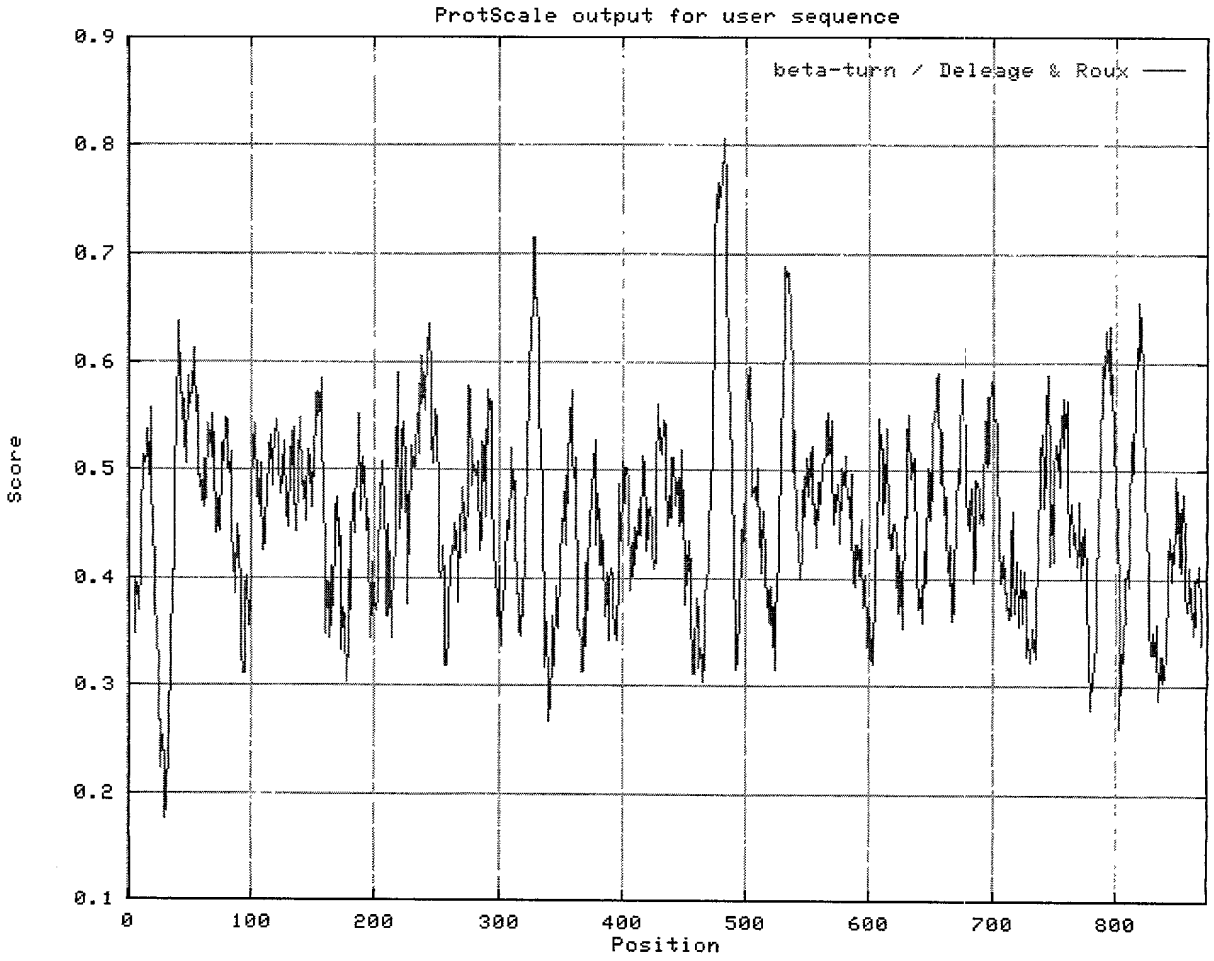


Figure 10: Expression of 161P2F10B by RT-PCR

M = Marker
- Vital Pool 1
2) Vital Pool 2
3) Xenograft Pool
4) Prostate Cancer Pool
- Kidney Cancer Pool
- Colon Cancer Pool
- Lung Cancer Pool
- Ovary Cancer Pool
- Breast Cancer Pool
- Metastasis Pool
- Pancreas cancer Pool
- Prostate Met to LN #1
- Prostate Met to LN #2

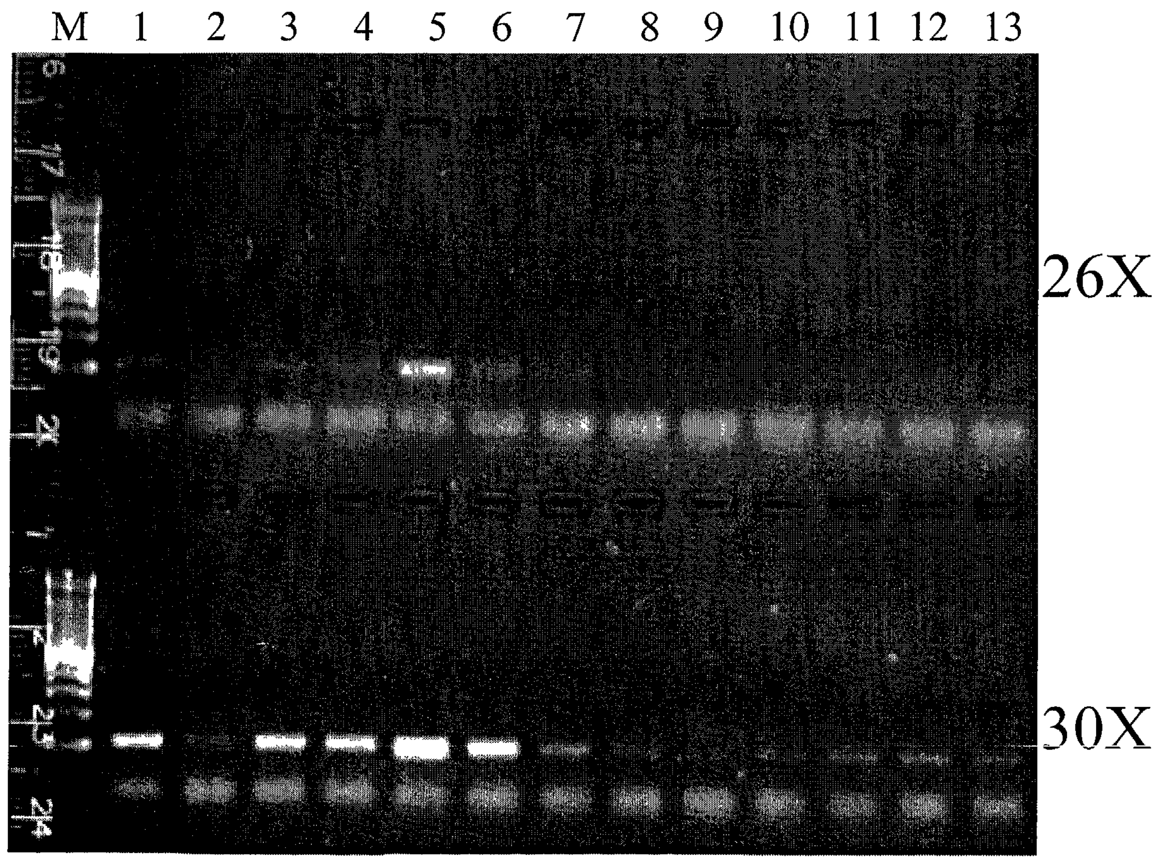
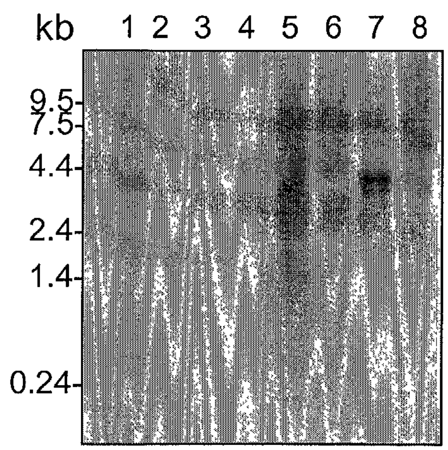
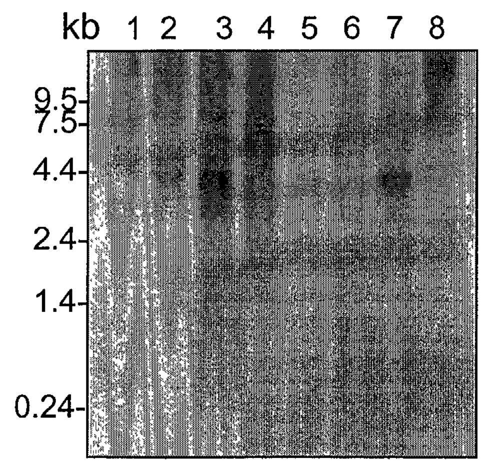


Figure 11: Expression of 161P2F10B in Normal Tissues

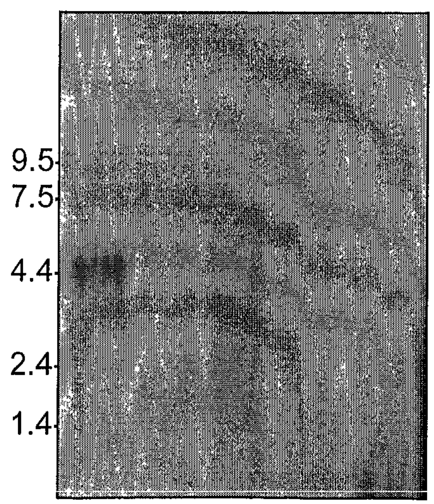


1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas



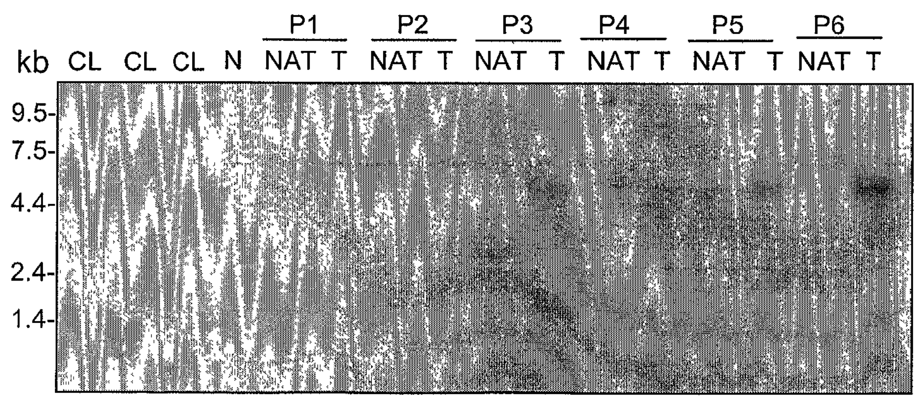
1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

Figure 12: Expression of 161P2F10B in Patient Kidney Cancer Specimens and in Normal Tissues



KCP = Kidney Cancer Poll
NP = Normal Prostate
NB = Normal Bladder
NK = Normal Kidney
NC = Normal Colon

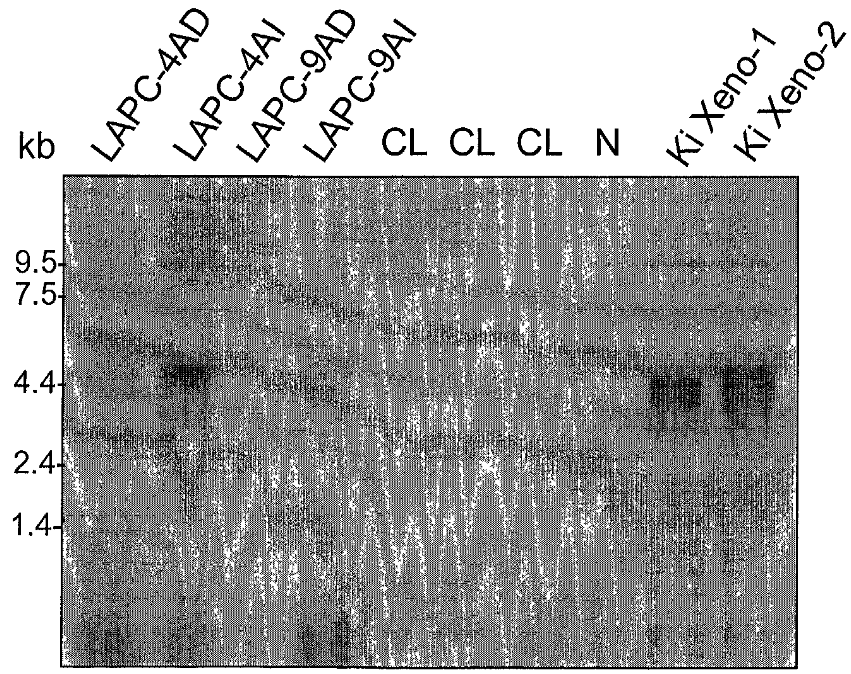
Figure 13: Expression of 161P2F10B in Kidney Cancer Patient Specimens



CL = cell lines listed in order: 769-P, A498, SW839
N = Normal kidney
NAT = Normal adjacent tumor
T = Tumor
P = Patient

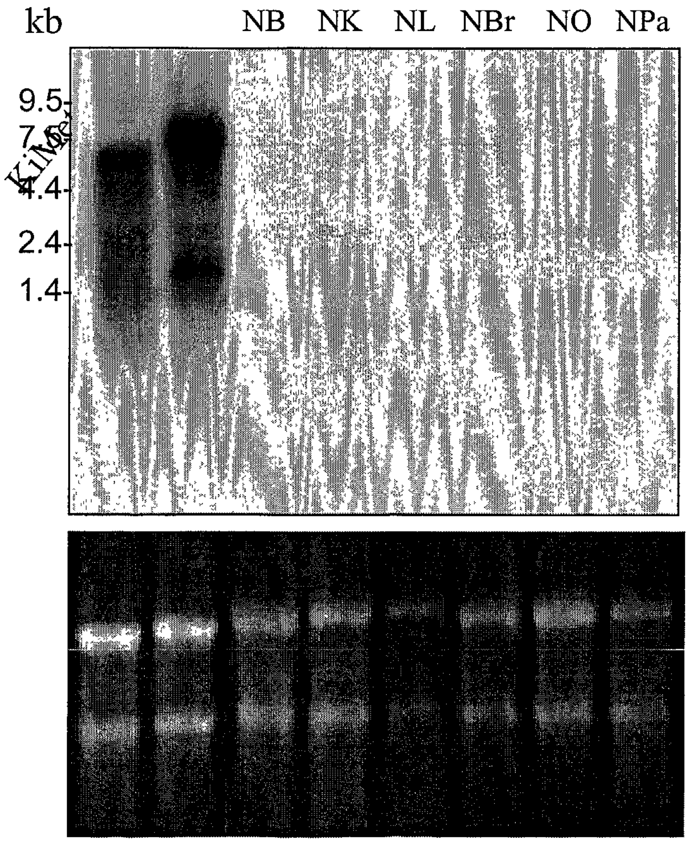
P1 - Papillary carcinoma, stage I
P2 - Invasive papillary carcinoma
P3 - Clear cell type grade 1/3, focally 2/3
P4 - Clear cell type, stage III
P5 - Clear cell type, stage III
P6 - Clear cell type, stage III

Figure 14: Expression of 161P2F10B in Kidney Cancer Xenografts



CL = cell lines listed in order: 769-P, A498, Caki-1
N = Normal kidney
Ki Xeno = Kidney xenograft

Figure 15: Expression of 161P2F10B in Kidney Cancer Metastasis Specimens and in Normal Tissues



KiMet 1 = Kidney Metastasis to lung
KiMet 2 = Kidney Metastasis to lymph node
NB = Normal Bladder
NK = Normal Kidney
NL = Normal Lung
NBr = Normal Breast
NO = Normal Ovary
NPa = Normal Pancreas

Figure 16: Expression of 161P2F10B Protein by Immunohistochemistry in Kidney Cancer Patient Specimens

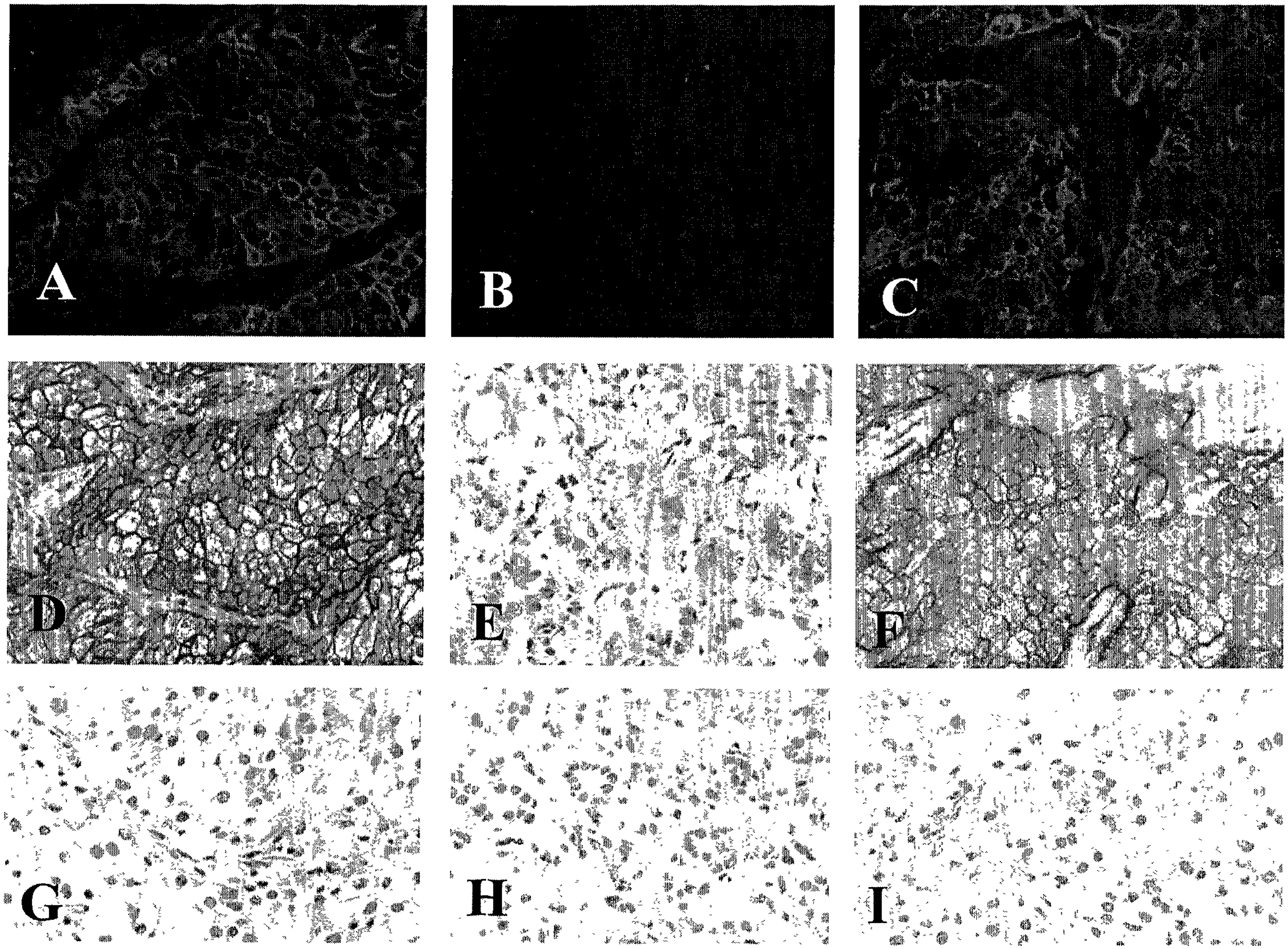
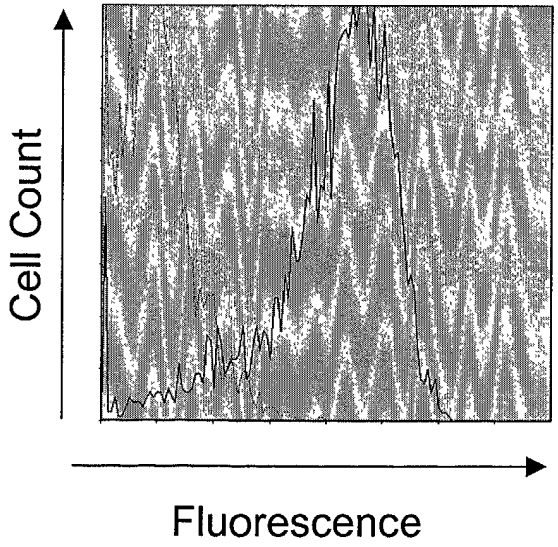


Figure 17: Expression of 161P2F10B Protein on the Cell Surface of Renal Cell Carcinoma Xenografts

A. Clear Cell Carcinoma



B. Renal Cancer Metastasis to LN

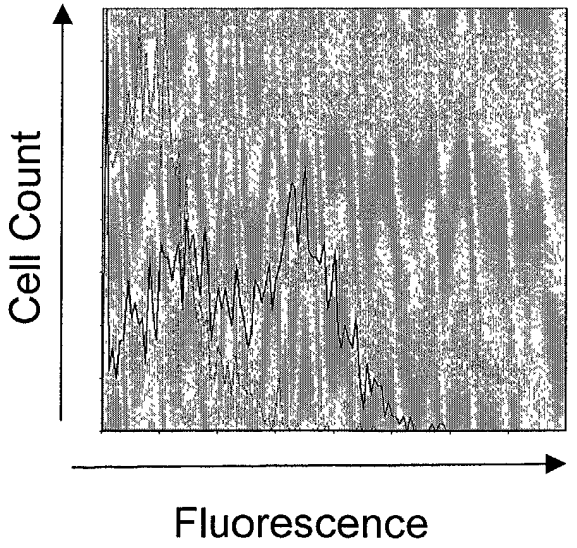


Figure 18: Expression of 161P2F10B Protein by Immunohistochemistry in Human Cancer Xenograft Tissues

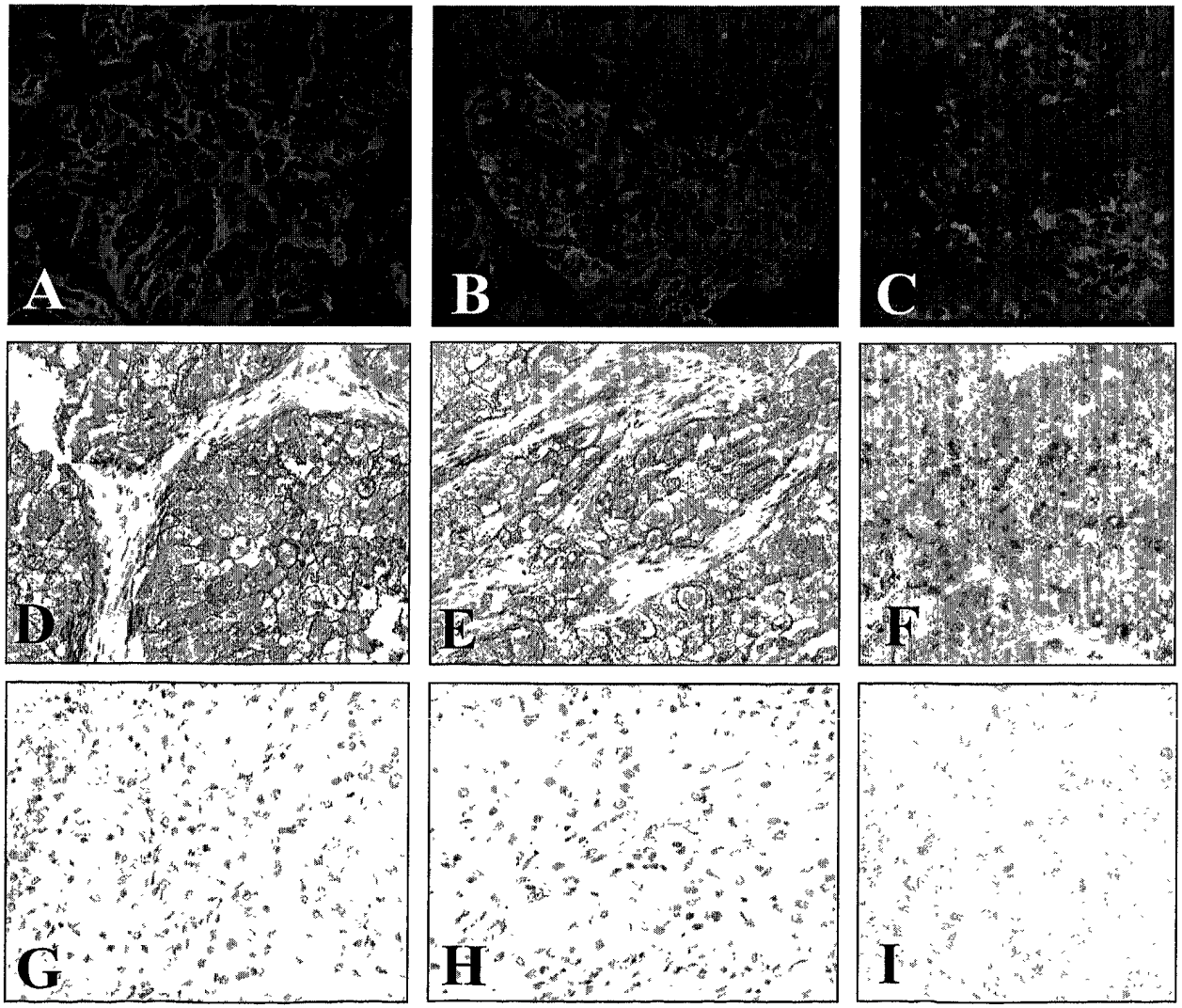
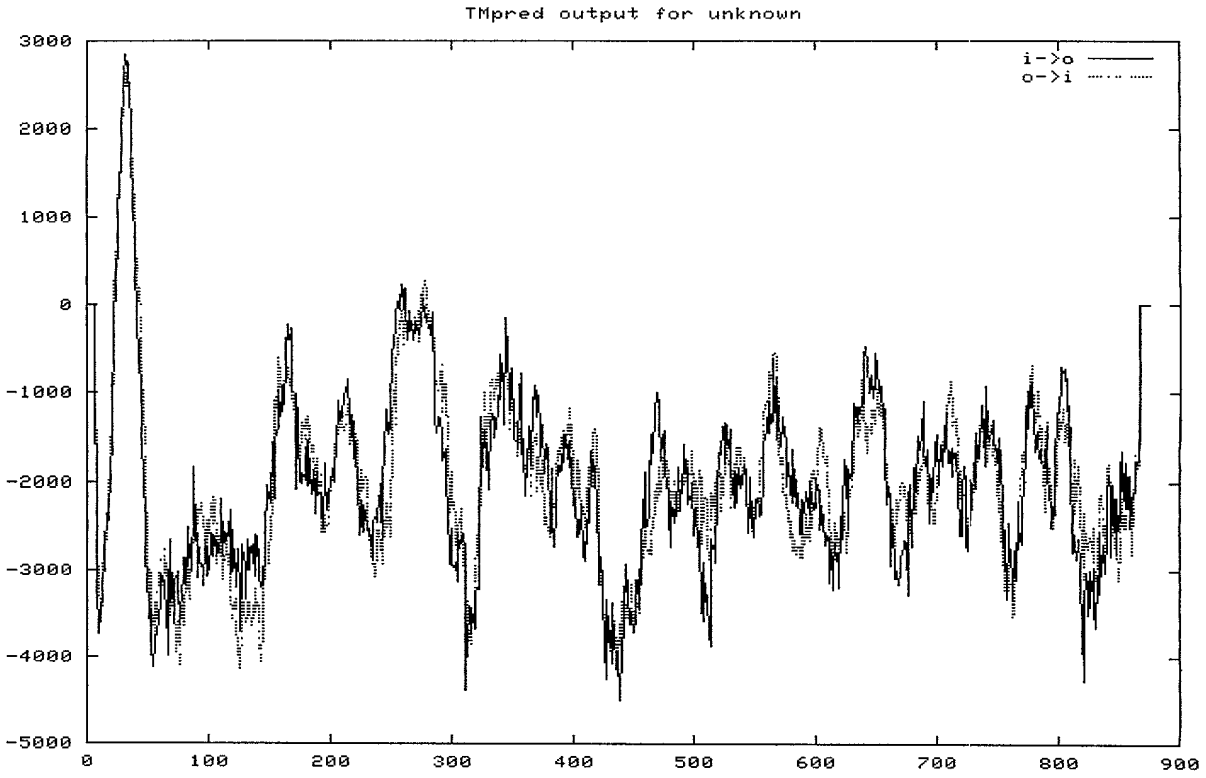


Figure 19A

```
         10        20        30        40        50        60        70
         |         |         |         |         |         |         |
MESTLTLATEQPVKKNTLKKYKIACIVLLALLVIMSLGLGLGLGLRKLEKQGSCRKKCFDASFRGLENCR
ccceeeeeccccccccchhhhhhhhhhhhhhhhhhhhhchhhhhhhhhhhcccccccccccccccchhcccc
CDVACKDRGDCCWDFEDTCVESTRIWMCNKFRCGETRLEASLCSCSDDCLQKKDCCADYKSVCQGETSWL
ccccccccccccccccccchhhhhehhhhhcccccceeechccccccccccccccccccccccccccch
EENCDTAQQSQCPEGFDLPPVILFSMDGFRAEYLYTWDTLMPNINKLKTCGIHSKYMRAMYPTKTFPNHY
ccccccccccccccccccceeeeeccccchhhhhhhhhhhhchhhhcccccchhhhheeccccccccccce
TIVTGLYPESHGIIDNNMYDVNLNKNFSLSSKEQNNPAWWHGQPMWLTAMYQGLKAATYFWPGSEVAING
eeeeeccccccchhcccccccccccceeeccccccccccccchhhhhhhhhcccceeeeccccceeeecc
SFPSIYMPYNGSVPFEERISTLLKWLDLPKAERPRFYTMYFEEPDSSGHAGGPVSARVIKALQVVDHAFG
ccceeeccccccchhhhhhhhhhhhcccccccceeeeeeccccccccccchhhhhhhhhhhhhhhhh
MLMEGLKQRNLHNCVNIILLADHGMDQTYCNKMEYMTDYFPRINFFYMYEGPAPRIRAHNIPHDFFSFNS
hhhhhhhhhhcccceeeeeeeccccccccccchhhhhhhcccceeeeeeeccccccccccccccchhhcch
EEIVRNLSCRKPDQHFKPYLTPDLPKRLHYAKNVRIDKVHLFVDQQWLAVRSKSNTNCGGGNHGYNNEFR
hhhhhhhccccccccccccccccchhhhhhcccccchhhhhhhhhhheeeccccccccccccccchhhh
SMEAIFLAHGPSFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEPSHAEEVSKFS
hhhhhhhhcccccccccccccchhhhhhhhhhhhhcccccccccccccchheeccccccccccchccee
VCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLPFGRPRVLQKNVDHCLLYHREY
eeccccccccccchhhcccccccchhhhhhhhhhhchhhhhheeeeccccccccehccccccceeeehhhh
VSGFGKAMRMPMWSSYTVPQLGDTSPLPPTVPDCLRADVRVPPSESQKCSFYLADKNITHGFLYPPASNR
hhccccceeeccccccccccccccccccccccccccccccccccccccccceeeeccccccccccccccc
TSDSQYDALITSNLVPMYEEFRKMWDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLA
ccchhhhhhhhhhcccchhhhhhhhhhhhhhhhhhehhccccccceeeccccccccccccchhhhhhhhcc
NTDVPIPTHYFVVLTSCKNKSHTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVR
ccccccccceeeeeeeeccccccccccccccccccceeeeccccccccccccccchhhhhhhhhhhhhhhh
DVELLTGLDFYQDKVQPVSEILQLKTYLPTFETTI
hheehccccccchcchhchhhhhehhhhcccccccc
```

c: random coil (31.31%)
e: extended strand (11.31%)
h: alpha helix (57.37%)

Figure 19B


TMpred output for unknown
i->o
o->i
3000
2000
1000
0
-1000
-2000
-3000
-4000
-5000
0
100
200
300
400
500
600
700
800
900

C

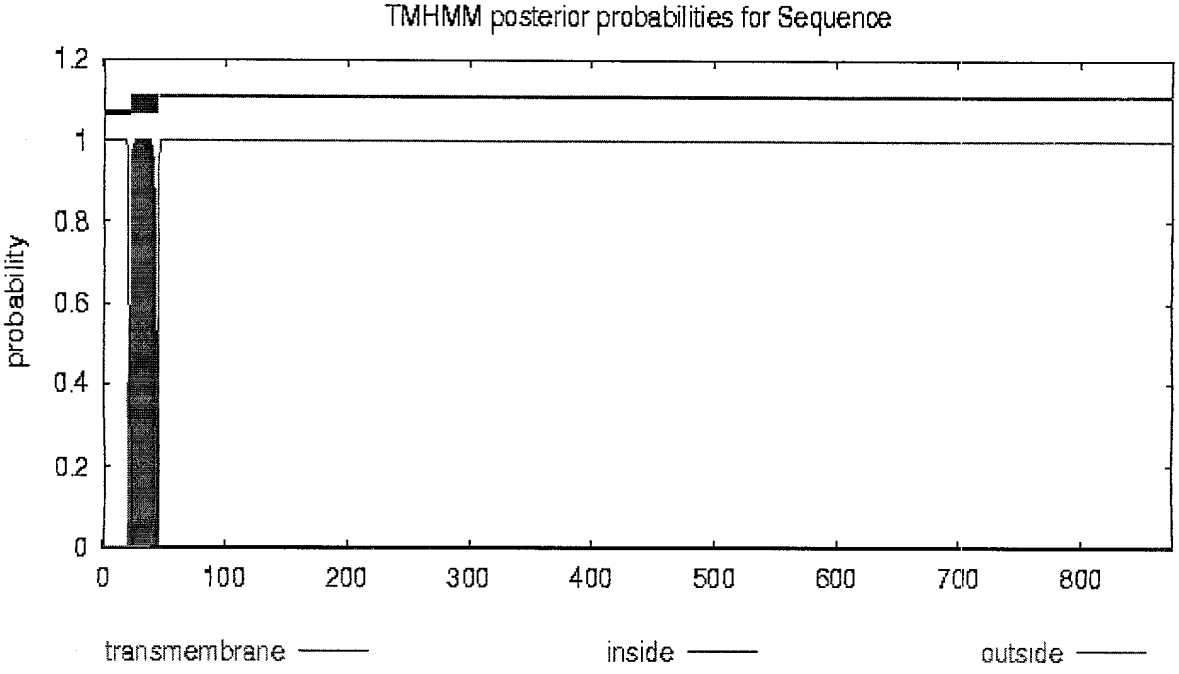
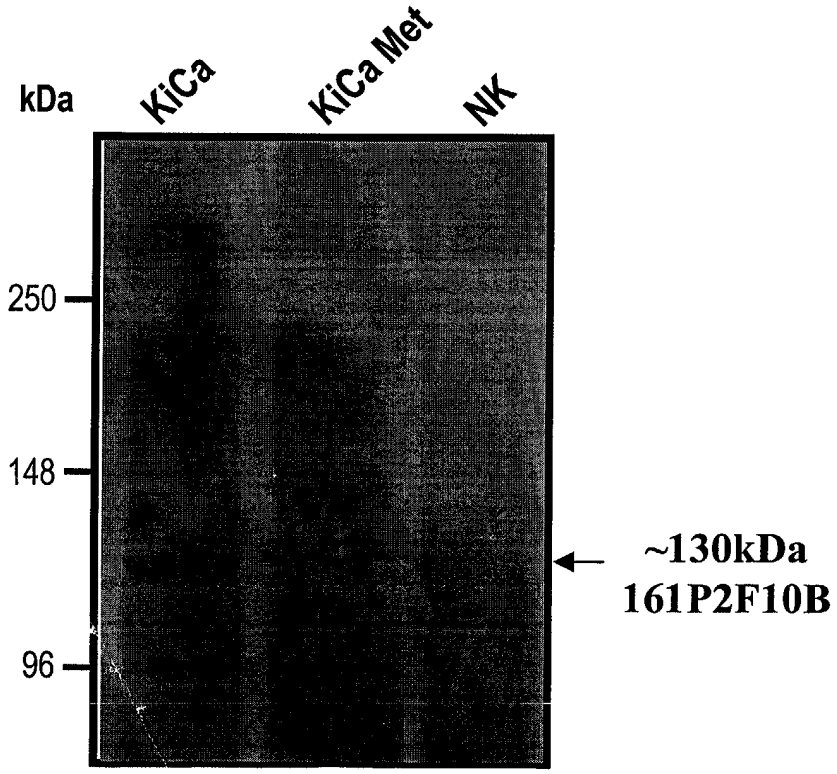
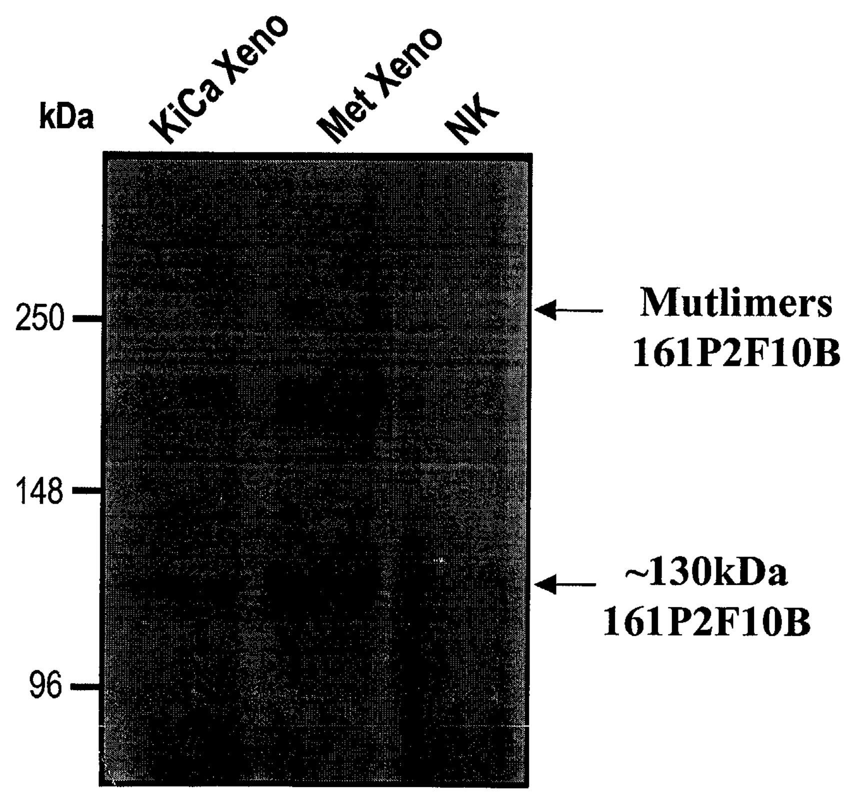

TMHMM posterior probabilities for Sequence
probability
1.2
1
0.8
0.6
0.4
0.2
0
0
100
200
300
400
500
600
700
800
transmembrane
inside
outside

Figure 20 Expression of 161P2F10B in Human Patient Cancers by Western Blot



KiCa = Kidney cancer, clear cell carcinoma
KiCa Met = Kidney cancer metastasis to lymph node
NK = Normal kidney

Figure 21 **Expression of 161P2F10B in Human Xenograft Tissues by Western Blot**



KiCa Xeno = Xenograft of kidney cancer, clear cell carcinoma
Met Xeno = Xenogrraft from Kidney cancer metastasis to lymph node
NK = Normal kidney